

Language	Written	Oral
Hindi :	Excellent	Excellent
French :	Nil	Nil

Qualification Details

Highest Degree: Ph.D.

University :

Specilization

Year: 2011

Expected/Anticipated dates of departure and return (if Awarded)

Departure date from India/Canada :2019-06-01

Return date from Canada/India :2019-06-29

Details of Project/Program/Abstract/Ethics

Project Title:

Objectives of Project/Program: The main goal of this visit is to learn and analyze the metagenomic data which I have collected in India from several plants rhizosphere including Soyabean, jatropha, Madhuca indica, Deodara, termites degraded Butea monosperma, lantana, parthenium, and the data that have been collected from the Madhya Pradesh through DBT funded project entitled “Mapping and quantitative assessment of plant resources and its distribution in Madhya Pradesh, Central India”. The main goal of our research to analyze the plant microbiome of different habitat by using Next generation sequencing approach and taxonomically and functionally assign the role of microbial community in governing belowground and aboveground phenomenon. Although very limited work has been done on this aspect, therefore, we are trying to unravel the hidden information by using the power of different bioinformatic software’s available with Prof. _____ and by using his expertise. We already have sequenced data that have been collected from several field sites by standard procedure of sampling to sequencing.

Background and Rationale of Project/Program(300 words): The trillions of microbes that colonize and live around us govern the health of both plants and animals through a cascade of direct and indirect mechanisms. Understanding this enormous and largely untapped microbial diversity has been the focus of microbial research from past few decades or so. Amidst the advancements in sequencing technologies, significant progress has been made to taxonomically and functionally catalogue these microbes and to establish their exact role in the health and diseases state. In comparison to the human microbiome, plants are also surrounded by vast diversity of microbes that form complex ecological communities that affect plant growth and health through collective metabolic activities and interactions. This plant microbiome has a substantial influence on human health and environment via its passage through nasal route and food chain, and responsible for changing our gut microbiome. Plant-associated microbial communities stimulate the

plant growth and increase their resistance to various stresses and diseases. Linking the distribution of microbial diversity and ecosystem functioning is essential to understand ecosystem responses to a changing environment. Because of their important and undisputable roles in biogeochemical cycling, plant growth and carbon sequestration, soil microbial taxa are imperative in relation to global climate changes. Very less work has been done on plant microbiome till date, therefore in this research we are trying to explore the unseen microbial diversity found inside and outside of plants to unlock/unravel their role in governing the plant processes under various stress conditions. This is an novel attempt to characterize this largely untapped diversity and explore their function by using 16S rRNA amplicon approach and power of bioinformatic pipeline, that were unavailable before. Through this mobility program, Prof. Dayanandan would gave me training to analyse data by using softwares tools and establish the relationship between plant-microbe-environment.

Project/Program Details :(Please define (a) Scope, (b) Objectives, (c) Evidence of knowledge in the field, with citations and bibliography of relevant literature; (d) Social or practical relevance of the project; (e) Theories, methods and sources, (f) Preparatory work to be completed prior to commencement of fellowship (g) The need for carrying out the project in Canada/India. (2000 words max):

The main purpose of this visit is to learn and analyze the metagenomic data which I have collected in India from several plants rhizosphere including soyabean, jatropha, *Madhuca indica*, Deodara, termites degraded *Butea monosperma*, lantana, parthenium, and the data that have been collected from the Madhya Pradesh through DBT funded project entitled "Mapping and quantitative assessment of plant resources and its distribution in Madhya Pradesh, Central India". For the collection of data our research team has collected samples from different field and extracted whole genomic DNA, which have been amplified by using 16S rRNA primer and sequenced by Illumina MiSeq (Next Generation Sequencer). The main goal of this work is to taxonomically and functionally characterized the microbial samples by using culture independent approach, as only 1% of microbes can be cultured. Though I have some basic training in analyzing data but Prof. Dayanandan (Canadian Host) is an expert of community phylogenetics and well versed in using several modern tools and software related to this. Through this program, I will get good exposure by using Insilico analysis of this collected data with the help of Prof.] . At present we are designing collaborative project, and some joint publication will come out by this collaboration. Research Students, M.Sc. and Postdoc students would be benefited by this mobility.

Title:

Introduction: The trillions of microbes that colonize and live around us govern the health of both plants and animals through a cascade of direct and indirect mechanisms. Understanding this enormous and largely untapped microbial diversity has been the focus of microbial research from past few decades or so. Amidst the advancements in sequencing technologies, significant progress has been made to taxonomically and functionally catalogue these microbes and to establish their exact role in the health and diseases state. In comparison to the human microbiome, plants are also surrounded by vast diversity of microbes that form complex ecological communities that affect plant growth and health through collective metabolic activities and interactions. This plant microbiome has a substantial influence on human health and environment via its passage through nasal route and food chain, and responsible for changing our gut microbiome. Plant-associated microbial communities stimulate the plant growth and increase their resistance to various stresses and diseases. Linking the distribution of microbial diversity and ecosystem functioning is essential to understand ecosystem responses to a changing environment. Because of their important and undisputable roles in biogeochemical cycling, plant growth and carbon sequestration, soil microbial taxa are imperative in relation to global climate changes. Modern genomic approaches shows tremendous potential for identifying uncultivated diversity, finding shifts in the bacterial community associated with sensitive and disease tolerant plants, and understanding how microbiota are affected by climate changes.

The main goal of our research to analyze the plant microbiome of different habitat by using Next generation sequencing approach and taxonomically and functionally assign the role of microbial community in governing belowground and aboveground phenomenon. Although very limited work has been done on this aspect, therefore, we are trying to unravel the hidden information by using the power of different bioinformatic software's available with Prof. and by using his expertise. We already have sequenced data that have been collected from several field sites by standard procedure of sampling to sequencing.

Methodology: I will analyze the microbiome data which I have collected from sequencing the total genomic DNA which we have extracted from soil samples by using standard DNA extraction, amplification and by Next generation Sequencing procedure. In this we have used 16S rRNA amplicon sequencing using Illumina MiSeq. The other parameters were already analyzed such as soil biochemical analysis, plant morpho-biochemical related parameters. The digital photographs of the habitat of each sample were taken, and coordinates of sampling locations were recorded and mapped. Several features including topographical (elevation, slope, aspect, soil type, soil color, humus), vegetation (physiognomy, stature, canopy cover) and climate data of each plot were recorded. **NG** Sequenced data has been submitted to the MG-RAST server with necessary metadata. The phylogenetic analysis will be performed using maximum parsimony and maximum likelihood methods using backbone-constrained tree. The software programs like Phylomatic, PAUP*, McClade and PHYLIP and many more will be used for the phylogeny reconstruction. Comparative Taxonomic and Functional Diversity for selected samples by QIIME by making use of PyCogent toolkit will be done. For comparative taxonomic profiling and annotation of the collected microbiome data will be carried out by QIIME release 1.9.1 using default parameters by Caporaso et al. (2010). The taxonomic profiling of the DNA samples extracted from the soil samples will be performed against RDP database with the default parameters and the phylotypes will be analyzed upto the genus level. In order to understand how the microbial communities interact with each other and with their plant hosts, future research should be focused more on the diversity and function. A number of bioinformatics analysis pipelines and software's are available that will help to process and analyze the data collected in this study, like QIIME, MOTHUR, MEGAN, MG-RAST, Galaxy portal, Functionalize R upto taxonomic and functional level. As Prof. Daya lab is working on plant community phylogenetics analysis, that would be beneficial to establish the link between the microbiome and plant and their role in governing plant functions under growth limited conditions.

Details of Ethics

Does your project require ethics approval due to research on human subjects, input on the environment, bio hazards etc.?

Note: Shastri Institute cannot release funds without a “Certificate of Ethics Approval” from your home institution

no

If yes, have you initiated the ethics approval process at your home institution?

no

Referee details

Names and addresses of two academicians who are giving letters of recommendation along with this application form. Letters of recommendation should explain the ‘referees’ professional relationship to the applicant and testify the competency of the applicant

Name and designation with complete address of first academicians(First) :

Name and designation with complete address of Second academicians(Second) :

Details activities schedule in India or Canada

Please enlist the activities, meetings with people, institutions to be visited from Day one to the last day of stay of the award/fellowship in India or Canada :

• 02 June, 2019 - Arrival at Montreal. • 03 June, 2019 – Reporting at Biology Department, Concordia University and complete the official formalities. • 04 June, 2019 – Discussion with Prof. S. Dayanandan, collaborator about the project • 05- 25 June, 2019 – Laboratory work and analysis of Data • 26-28 June, 2019 – Writing of report • 29 June, 2019 – Departure from Montreal to India

Affiliate details

Proposed institution/university for affiliation (in order of preference) with details of the contact person: (Please seek prior consent from the affiliate before proposing name and obtain a formal invitation letter on the letterhead of his/her institution)

Name and designation with complete address of first Affiliate :

]

Name and designation with complete address of Second Affiliate :

Category Of Application (Academician/Administration) Details

category of Shastri Mobility Programme applied for:Academic faculty

Passport Details

Note: Passport is mandatory to avail the fellowship. Those who do not have passport at the time of submitting application kindly submit an affidavit stating the they will submit the copy of passport within one month post deadline.

Passport Number If Having or Put NA:J6693428

Expiry Date of Passport:2021-03-03

View Details of purpose of visit

Please choose the purpose applicable in your case and providing a concise description the purpose opted to visit to Canadian/Indian Institutions :TF

A. Internationalization of the curriculum/teaching and understand the recent developments in Canada/IndiaNo

B. To learn new advanced pedagogy of the discipline in India or Canada;No

C. Delivering lectures and talk as an specialist in the discipline of expertise in institutions in India or Canada relevant to SICI focus areas and priority areas of MHRD, Govt. of IndiaNo

D. To carry out small Research Project of 2-3 weeks duration in collaboration with Indian or Canadian faculty;Yes

E. Top attend Seminar/workshop related to the subject that you are currently teaching in your institution;No

Concise description the purpose opted to visit to Canadian/Indian Institutions. (2,000 words)

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Evaluation Criteria

- The strength of the applicant's academic/professional record (10 points)
- The feasibility of the project as designed (10 points)
- The clear demonstration of necessity to carry out the work in Canada (10 points)
- The potential contribution of the applicant to the area of academics (10 points)
- Strategies for dissemination of project outcomes(10 points)

